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ABOUT THE COVER

Understanding endocrine therapy–resistant breast cancer is of major clinical importance. Therefore, a comparative bioinformatics analysis of the Cancer Cell Line Encyclopedia (CCLE) and The Cancer Genome Atlas (TCGA) datasets was performed to identify genes whose expression is highly associated with the proto-oncogene AGR2. From the genes identified, the transcription factor FOXA1 was significantly associated. The cover image summarizes the CCLE correlation represented by size, with larger circles predicting higher co-expression and TCGA correlation represented based on color, Red>Purple>Blue>White. Please see the article by Wright and colleagues (beginning on page 1829) for more information.



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